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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/701,926	06/01/2001	Bernard John Carroll	99977-410	1281

28089 7590 06/03/2003

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EXAMINER
COLLINS, CYNTHIA E

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 06/03/2003

17

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/701,926	CARROLL, BERNARD JOHN	
	Examiner	Art Unit	
	Cynthia Collins	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *03 March 2003* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-22* is/are pending in the application.

4a) Of the above claim(s) *10-19 and 22* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-9,20 and 21* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *6* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Election/Restrictions

Applicant's election with traverse of Group I, claims 1-9 and 21-22, and SEQ ID NO:1, in Paper No. 16 is acknowledged. The traversal is on the ground(s) that at least the claims of Groups I and II should be examined together because they relate to methods of affecting or modulating the expression of a nucleotide sequence, such that they form a general inventive concept and share a common technical feature as required under PCT Rules 13.1 and 13.2 (reply page 2). Applicant also argues that a search of Groups I and II would not impose an undue burden on the Office (reply page 3). Applicant additionally argues that the species election of one SEQ ID NO: should apply only to claim 20, as only claim 20 recites specific sequences (reply page 3). Applicants further argue that it would not be an undue burden to search all of the specific sequences as they all comprise a phenotype modulating genetic sequence, and Applicant additionally points out that MPEP 803.04 indicates that normally 10 sequences constitute a reasonable number of sequences for examination purposes (reply pages 3-4).

This is not found persuasive because the technical feature linking Groups I and II does not constitute a special technical feature as defined by PCT Rule 13.2, because it does not define a contribution over the prior art. If the technical feature linking different groups of invention does not constitute a special technical feature, there is not unity of invention. This is also not found persuasive because while the searches of Groups I and II may overlap, their searches are not coextensive of each other. In this particular instance, a search of Group II is not coextensive with a search of Group I, since Group II requires a search for methods not claimed in Group I. Additionally, this is not found persuasive because while only claim 20 recites specific sequences,

all the groups of invention are linked by a phenotype modulating genetic sequence. Furthermore, the restriction requirement mailed October 3, 2002 made no requirement for an election of species. As stated at page 2 of the restriction requirement, "restriction to one of SEQ ID NOS: 1-31 is also required under 35 U.S.C. 121 and 372". Applicant is reminded that nucleotide sequences are structurally distinct chemical compounds and are unrelated to one another. These sequences are thus deemed to normally constitute **independent and distinct** inventions within the meaning of 35 U.S.C. 121. Absent evidence to the contrary, each such nucleotide sequence is presumed to represent an independent and distinct invention, subject to a restriction requirement pursuant to 35 U.S.C. 121 and 37 CFR 1.141 et seq. This requirement is not to be construed as a requirement for an election of species, since each nucleotide sequence is not a member of a single genus of invention, but constitutes an independent and patentably distinct invention. With respect to the indication at MPEP 803.04 that normally 10 sequences constitute a reasonable number of sequences for examination purposes, database and resource allocations at the PTO are currently such that a search of more than one distinct sequence in the instant application would present a burden on PTO resources. Accordingly, claims 10-19 and 22, and the nonelected sequences, are withdrawn from consideration as being directed to nonelected inventions.

The requirement is still deemed proper and is therefore made FINAL.

Information Disclosure Statement

An initialed and dated copy of Applicant's IDS form 1449, filed August 13, 2001, Paper No. 6, is attached to the instant Office action.

Specification

This application does not contain an abstract of the disclosure as required by 37 CFR 1.72(b). An abstract on a separate sheet is required.

The specification is objected to because the sequences are not referred to by use of the sequence identifier, preceded by "SEQ ID NO:", in the text of the description or claims, as required by 37 CFR 1.821(d). Appropriate correction is required.

Claim Objections

Claim 20 is objected to for reciting the sequences of nonelected inventions. Claim 20 is also objected to because the sequences are not referred to by use of the sequence identifier, preceded by "SEQ ID NO:", in the text of the claims, as required by 37 CFR 1.821(d). Appropriate correction is required.

Claims 7-8 are objected to under 37 CFR 1.75(c) as being in improper form because a multiple dependent claim cannot depend upon another multiple dependent claim, i.e. claim 5. See MPEP § 608.01(n). In the interest of compact prosecution, the claims will be examined. Such treatment does not relieve Applicant of the responsibility to respond to this objection.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-9 and 20-21 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to an isolated PMGS sequence, including any sequence of any structure which increases or stabilizes expression of any second proximal nucleotide sequence, any sequence of any structure that promotes de-methylation or prevents or inhibits methylation of a second nucleotide sequence, any sequence of any structure that modulates expression of an α-amylase gene, any sequence of any structure that encodes an α-amylase, any sequence of any structure that modulates expression of *Dem*, and an isolated PMGS sequence having at least 25% similarity to SEQ ID NO:1.

With respect to the sequence of the elected invention, SEQ ID NO:1, the specification describes only an isolated nucleic acid of SEQ ID NO:1, which is identified as being the nucleotide sequence of a tomato α-amylase gene promoter (page 24 Table 1). The specification does not characterize the isolated nucleic acid of SEQ ID NO:1 as having other functional properties, such as promoting de-methylation or preventing or inhibiting methylation of a second nucleotide sequence, or encoding an α-amylase, or modulating expression of *Dem*. The specification also does not describe any sequence having at least 25% similarity to SEQ ID NO:1 and having the functional properties set forth in the claims.

The Federal Circuit has recently clarified the application of the written description requirement. The court stated that a written description of an invention "requires a precise

definition, such as by structure, formula [or] chemical name, of the claimed subject matter sufficient to distinguish it from other materials." University of California v. Eli Lily and Co., 119 F.3d 1559, 1568; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The court also concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." Id. Further, the court held that to adequately describe a claimed genus, Patent Owner must describe a representative number of the species of the claimed genus, and that one of skill in the art should be able to "visualize or recognize the identity of the members of the genus." Id.

Given the claim breadth and lack of guidance as discussed above, the specification fails to provide an adequate written description of the genus as broadly claimed. Given the lack of written description of the claimed product, any method of using it would also be inadequately described. Accordingly, one skilled in the art would not have recognized Applicants to have been in possession of the claimed invention at the time of filing. See Written Description Requirement guidelines published in Federal Register/ Vol. 66, No.4/ Friday January 5, 2001/Notices: pp. 1099-1111).

Claims 1-9 and 20-21 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are broadly drawn to an isolated PMGS sequence, including any sequence of any structure which increases or stabilizes expression of any second proximal nucleotide

sequence, any sequence of any structure that promotes de-methylation or prevents or inhibits methylation of a second nucleotide sequence, any sequence of any structure that modulates expression of an α-amylase gene, any sequence of any structure that encodes an α-amylase, any sequence of any structure that modulates expression of *Dem*, and an isolated PMGS sequence having at least 25% similarity to SEQ ID NO:1. The claims are also drawn to a method of increasing or stabilizing the expression of a nucleotide sequence by using a PMGS sequence.

With respect to the sequence of the elected invention, SEQ ID NO:1, the specification discloses only an isolated nucleic acid of SEQ ID NO:1, which is identified at page 24 as being the nucleotide sequence of a tomato α-amylase gene promoter. Additionally, at page 41, the specification discloses that transposon tagging has been used to introduce a transposon into the tomato α-amylase gene. The specification does not, however, provide any evidence that an isolated nucleic acid of SEQ ID NO:1 has promoter function, or that an isolated nucleic acid of SEQ ID NO:1 has any of the other functional attributes recited in the claims. The specification also does not disclose the structure of function of sequences having at least 25% similarity to SEQ ID NO:1.

Guidance for making and using the claimed invention is necessary for enablement because the ability of any particular nucleotide sequence to function as a promoter is highly unpredictable. Sequences homologous to a promoter sequence also cannot predictably be assumed to have promoter activity. This unpredictability originates in the mechanics of promoter function, which requires the presence of particular nucleotides in the sequence to mediate promoter function. As a consequence, it is unpredictable whether any nucleotide sequence would have promoter function, because it is unpredictable whether any sequence would possess all the

particular nucleotides necessary to mediate promoter function. It is also unpredictable whether a sequence having at least 25% similarity to a promoter sequence would exhibit promoter function, because it is unpredictable whether a sequence having at least 25% similarity to a promoter sequence would retain all the particular nucleotides necessary to mediate specific promoter function.

For example, Kim et al. teach that various point mutations in the *nos* promoter can alter the presence or level of promoter activity in tobacco. (Plant Molecular Biology, 1994, Vol. 24, pages 105-117). Mutation of one or more nucleotides in either of two hexamer motifs or in the octamer spacer region between them significantly altered the level of *nos* promoter activity (Table 2, page 109). For example, a single point mutation in the sixth nucleotide of the hexamer motif resulted in a four to ten fold decrease in promoter activity, whereas a double point mutation in the fourth and fifth nucleotide of the hexamer motif resulted in a two-fold increase in promoter activity. Two independent triple point mutations in the third, fourth and fifth, and sixth, seventh and eighth nucleotides of the octamer spacer region eliminated detectable promoter activity. These mutant promoter sequences differ from the native promoter sequence by only one to three nucleotides in a region that spans only 20 nucleotides, yet they vary greatly in the ability to function as a promoter. This is because promoter function occurs through direct interaction between particular individual promoter nucleotides and the regulatory proteins that bind them.

Because promoter function is directly mediated by particular individual nucleotides, the function of a promoter may be more readily affected by a single nucleotide change than the function of a coding sequence, which can accommodate a variety of nucleotide changes without an effect on polypeptide function due to the degeneracy of the genetic code. Because promoter

function depends on the presence of particular individual nucleotides that interact with regulatory proteins to effect promoter function, the ability of any particular nucleotide sequence to function as a promoter is highly unpredictable. Because the ability of the claimed nucleic acid sequences to function as promoters in is not described by analogy or by working example, the claimed invention is not enabled by the specification in the absence of further guidance or example.

Guidance for making and using the claimed invention is also necessary because the ability of the claimed sequence, which is putatively designated as an α-amylase promoter sequence, to simultaneously function as an α-amylase promoter sequence, as an α-amylase coding sequence, and as a *Dem* promoter sequence is unpredictable. Such simultaneous functions are unpredictable because in eukaryotic organisms such as plants and animals, promoter sequences and coding sequences generally execute their functions separately and by different mechanisms. Eukaryotic promoter sequences function through direct interaction between particular individual promoter nucleotides and the regulatory proteins that bind them, whereas eukaryotic coding sequences function through the synthesis of an mRNA intermediate, which serves as a template for protein synthesis by interacting with ribosomes and tRNAs. Such simultaneous functions are also unpredictable because in eukaryotic organisms the expression of each specific coding sequence, such as an α-amylase coding sequence or a *Dem* coding sequence, is generally controlled by its own unique promoter sequence. Because of the unpredictability of a nucleic acid sequence simultaneously functioning as a promoter sequence for two distinct coding sequences and as a coding sequence, and because Applicant has not provided any evidence of any function for SEQ ID NO:1, the claimed invention is not enabled by the specification in the absence of further guidance or example.

Guidance for making and using the claimed invention is additionally necessary because the ability of the claimed sequence from a tomato plant to alter the expression of a nucleotide sequence in other species, such as animals, is unpredictable. The ability of a tomato plant promoter sequence to alter the expression of a nucleotide sequence in other species, such as animals, is unpredictable because the cells of other species do not necessarily contain proteins that can functionally interact with a particular promoter sequence obtained from tomato plants. The cells of other species, such as animals, may either lack proteins required to functionally interact with a particular tomato promoter sequence, or their proteins may not have sufficient homology with corresponding tomato proteins to functionally interact with the promoter. For example, Doelling et al. teach that in animals, rRNA promoters display little sequence similarity between species, and generally do not function across species (Nucleic Acids Research, 1996, Vol. 24, No. 23, pages 4725-4732, see page 4725 paragraph spanning columns 1 and 2). Doelling et al. also teach that in *Arabidopsis* protoplasts, a tomato RNA polymerase I promoter sequence initiates RNA polymerase I transcripts from a +32 transcription initiation position, rather than from a +1 transcription initiation position as in the native species (page 4739 Figure 3). Because of the unpredictability of a promoter sequence from one species functioning in another species, and because Applicant has not provided any evidence of any function for SEQ ID NO:1 in any species, the claimed invention is not enabled by the specification in the absence of further guidance or example.

Guidance for making and using the claimed invention is further necessary because the use of a nucleic acid sequence to prevent or reduce gene silencing or to promote transcription degradation is unpredictable. Preventing or reducing gene silencing or promoting transcription

degradation is unpredictable because such processes are multifactorial processes for which the underlying mechanisms have not been fully elucidated. For example, Montgomery et al. teach that a variety of different mechanisms have been proposed to explain gene silencing in plants (Trends in Genetics, July 1998, Vol. 14, No. 7, pages 255-258, see page 257 paragraph spanning columns 1 and 2). Montgomery et al. also teach that not all transgenes can cause co-suppression in plants, and that there is no basis for predicting which transgenes would have this effect (page 257 column 1 last paragraph). Montgomery et al. additionally teach that in some cases co-suppression is correlated with a high-level of transgene transcription, but in other cases, i.e. inversely repeated transgenes, there is no correlation with the level of transgene transcription and co-suppression (page 257, column 2, first full paragraph). Montgomery et al. further teach that a variety of different mechanisms have also been proposed to account for gene silencing observed in vertebrates and in other animal systems (page 258 column 2 second paragraph). Because of the unpredictability of using a nucleic acid sequence to prevent or reduce gene silencing or to promote transcription degradation, and because Applicant has not provided guidance with respect to how to use SEQ ID NO:1 to prevent or reduce gene silencing or to promote transcription degradation, the claimed invention is not enabled by the specification in the absence of further guidance or example.

Given the claim breadth, unpredictability, and lack of guidance as discussed above, it would require undue experimentation for one skilled in the art to determine whether the claimed nucleic acid sequences or variants exhibit promoter function, α-amylase encoding function, or *Dem*-modulating function, or whether the claimed nucleic acid sequences or variants could be

used to prevent or reduce gene silencing or to promote transcription degradation in plants or in animals.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-9 and 20-21 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Dependent claims are included in all rejections.

Claim 1 is indefinite in the recitation of "said first mentioned nucleotide sequence", as there is insufficient antecedent basis for "said first mentioned nucleotide sequence" in the claim.

Claim 1 is indefinite in the recitation of the preposition "of" to link "increases" and "stabilizes", which is confusing. If "and" or "or" were intended, appropriate correction is required.

Claims 3 and 6 are indefinite in the recitation of "modulates" expression. The term "modulates" is a relative term, as "modulates" implies a gradual adjustment for keeping a process in proper measure or proportion, for which there is no comparative basis.

Claim 3 is indefinite in the recitation of "the gene encoding an amylase", as there is insufficient antecedent basis for "the gene encoding an amylase" in the claim.

Claim 4 is indefinite in the recitation of "wherein said PMGS encodes an amylase". It is unclear how a PMGS sequence could encode an amylase, as claim 1 from which claim 4 depends indicates that the PMGS sequence is a regulatory sequence, which ordinarily would not encode a polypeptide.

Claim 6 is indefinite in the recitation of "*Dem*". It is unclear what "*Dem*" designates, as an acronym may have more than one meaning.

Claim 9 is indefinite in the recitation of "promoting transcription degradation of an endogenous gene". It is unclear whether the method is meant to have a degradative effect on transcription alone, or whether the method is meant to have a degradative effect on both transcription and an endogenous gene.

Claim 20 is indefinite in the recitation of "low stringency conditions". It is unclear what conditions would yield the claimed nucleic acid molecules because those skilled in the art define "low stringency conditions" differently. Recitation of the hybridization temperature alone does not clarify the issue, as variables other than temperature are crucial to stringency. It is suggested that the claim be amended to recite specific hybridization conditions.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claim 20 is rejected under 35 USC 101 because the claimed invention is directed to non-statutory subject matter.

Claim 20, as written, does not sufficiently distinguish over nucleic acids as they exist naturally, because the claim does not particularly point out any non-naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See Diamond v. Chakrabarty, 447 U.S. 303, 206 USPQ 193 (1980). The claim should be amended to indicate the hand of the inventor, e.g., by insertion of "Isolated" or "Purified".

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 3-9 and 20-21 are rejected under 35 U.S.C. 102(b) as being anticipated by WO 96/12813 (published 02 May 1996, Applicant's IDS).

The claims are drawn to an isolated PMGS sequence which increases or stabilizes expression of a second proximal nucleotide sequence, including an isolated PMGS sequence that modulates expression of an α-amylase gene, an isolated PMGS sequence that modulates expression of *Dem*, and an isolated PMGS sequence having at least 25% similarity to SEQ ID

NO:1. The claims are also drawn to a method of increasing or stabilizing the expression of a nucleotide sequence by using a PMGS sequence.

WO 96/12813 teaches an isolated nucleic acid sequence that increases or stabilizes expression of an α-amylase gene and that has at least 25% similarity to SEQ ID NO:1, and a method of increasing or stabilizing the expression of a nucleotide sequence (page 2 line 10 to page 3 line 17; Figure 4). While WO 96/12813 does not explicitly teach that the isolated nucleic acid sequence set forth in Figure 4 "modulates expression of *Dem*", the isolated nucleic acid sequence set forth in Figure 4 would inherently modulate the expression of any nucleic acid to which it is operatively linked, as the isolated nucleic acid sequence set forth in Figure 4 is a promoter sequence.

Claims 1-3 and 5-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Ronemus et al. (Science, 2 August 1996, Vol. 273, pages 654-657).

The claims are drawn to an isolated PMGS sequence which increases or stabilizes expression of a second proximal nucleotide sequence, including an isolated PMGS sequence that promotes de-methylation or prevents or inhibits methylation of a second nucleotide sequence.

Ronemus et al. teach an isolated nucleic acid sequence that inhibits methylation of a second nucleotide sequence (page 654 Figure 1; page 655 Table 1). The isolated nucleic acid sequence taught by Ronemus et al. would necessarily increase or stabilize expression of any second proximal nucleotide sequence, including a heterologous α-amylase or *Dem* coding sequence, as the sequence taught by Ronemus et al. inhibits DNA methylation, and DNA methylation is known to decrease gene expression.

Claims 1 and 4-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Gausing et al. (U.S. Patent 5,498,832 issued March 12, 1996, Applicant's IDS).

The claims are drawn to an isolated PMGS sequence which increases or stabilizes expression of a second proximal nucleotide sequence, including an isolated PMGS sequence that encodes an α-amylase

Gausing et al. teach an isolated nucleic acid encoding an α-amylase (Figures 1 and 2). While Gausing et al. do not explicitly teach that the isolated nucleic acid encoding an α-amylase increases or stabilizes expression of a second proximal nucleotide sequence, the isolated nucleic acid sequence encoding an α-amylase taught by Gausing et al. would inherently increase or stabilizes expression of a second proximal nucleotide sequence, as the isolated nucleic acid sequence encoding an α-amylase taught by Gausing et al. meets all the structural limitations of the claims.

Remarks

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Cynthia Collins whose telephone number is (703) 605-1210. The examiner can normally be reached on Monday-Friday 8:45 AM -5:15 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on (703) 306-3218. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 for regular communications and (703) 308-4242 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

CC
June 1, 2003

DAVID T. FOX
PRIMARY EXAMINER
GROUP ~~180~~ 1638